

FIGURE 1

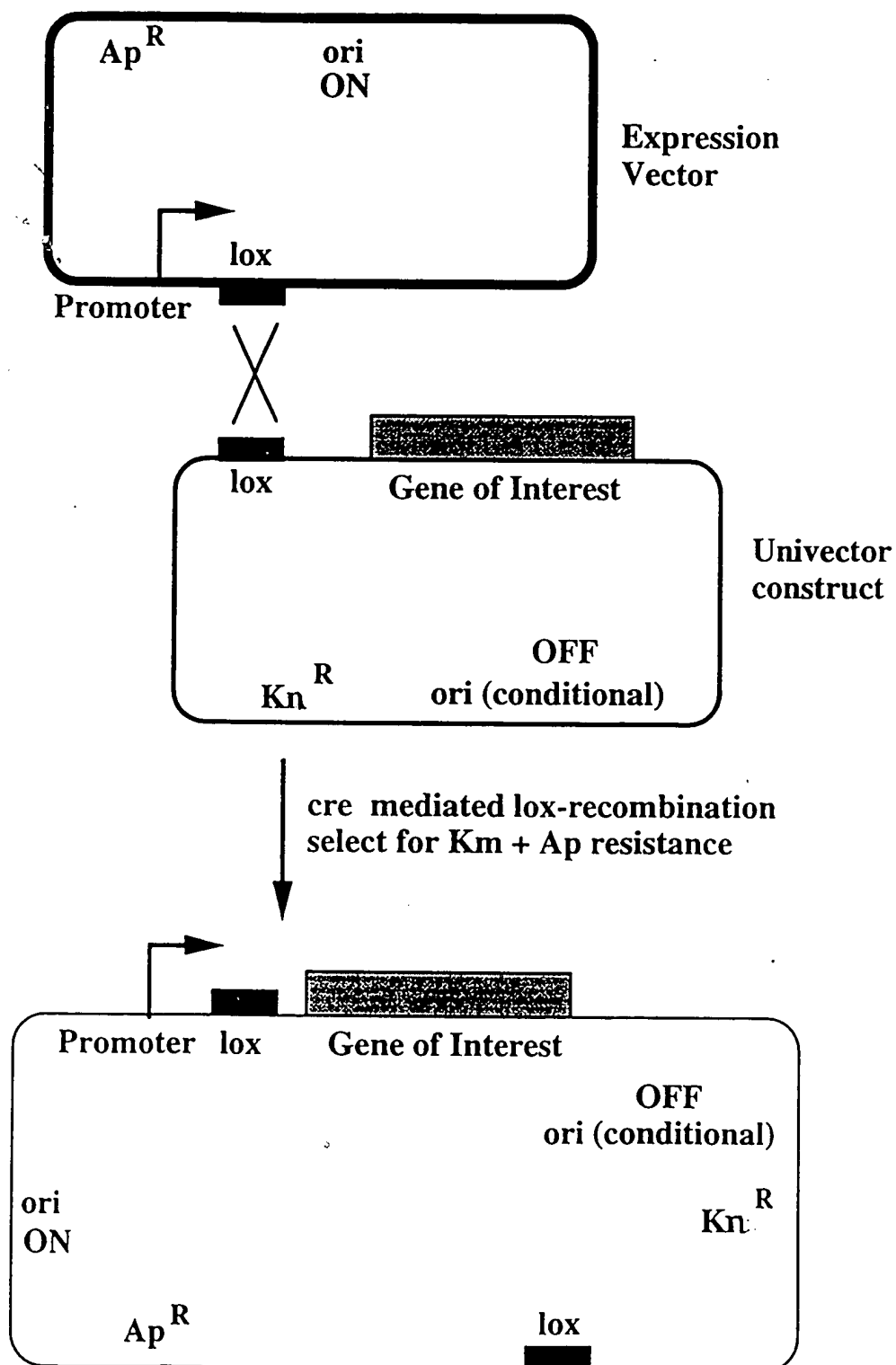
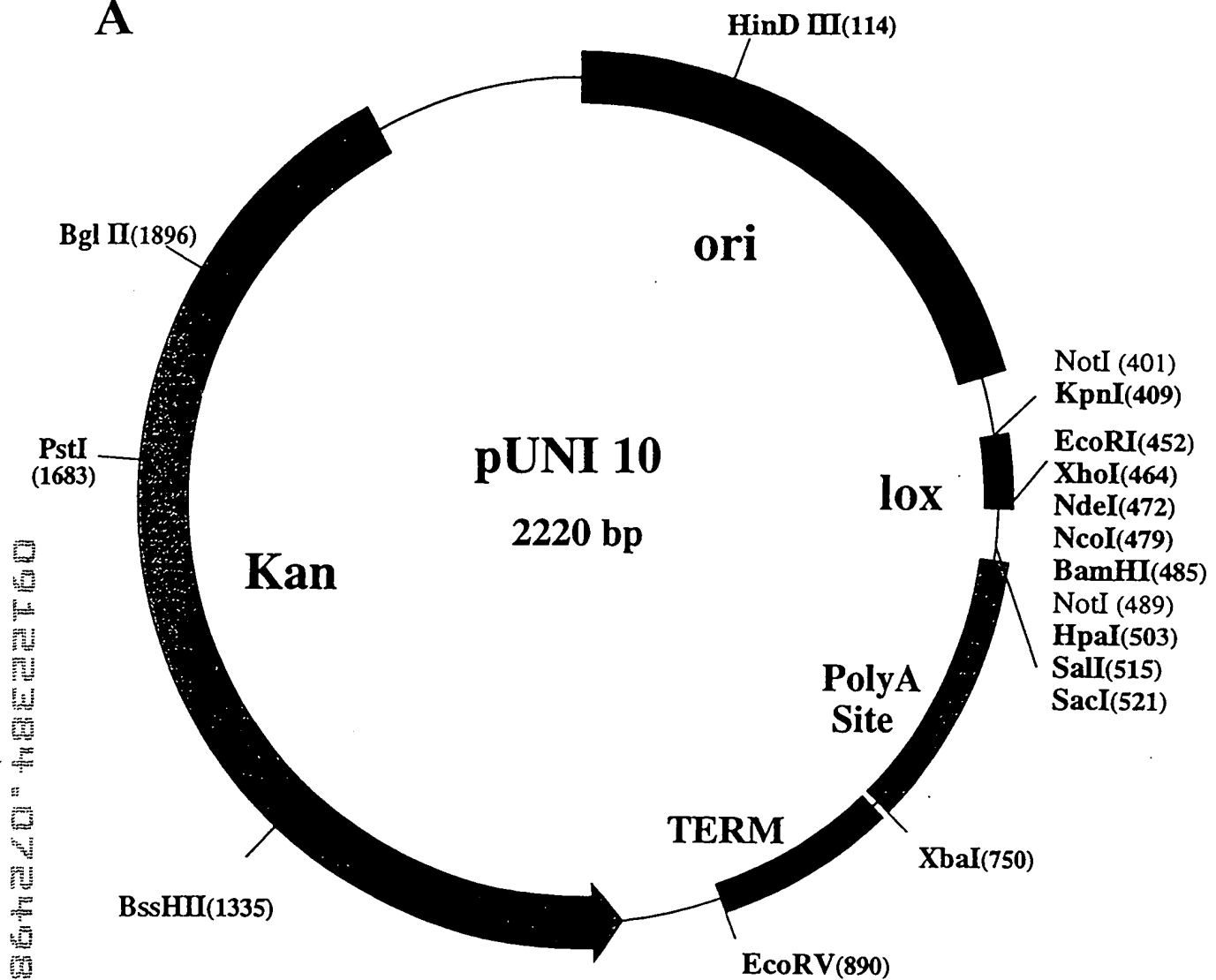


FIGURE 2

A



B

(401) NotI      KpnI      LOX

GC GGC CGC GGT ACC ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA TCT

EcoRI      SmaI      XhoI      NdeI      NcoI      BamHI      NotI

GGA ATT CCC CGG GCT CGA GAA CAT ATG GCC ATG GGG ATC CGC GGC CGC

HpaI      SalI      SacI

AAT TGT TAA CAG ATC CGT CGA CGA GCT CGC TA (530)

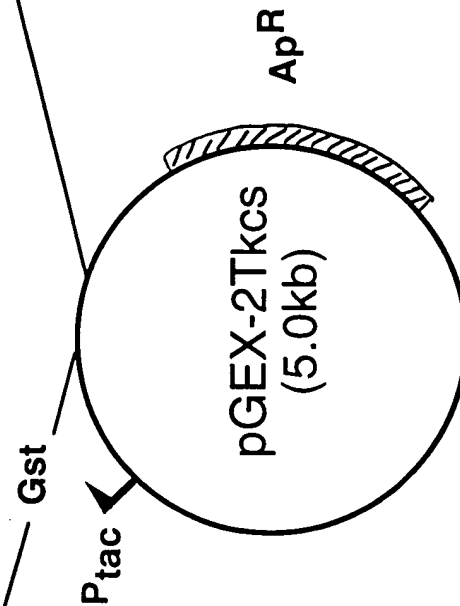
# Construction of pGst-lox:

A

Linker: C ATG GCT ATA ACT TCG TAT AGC ATA CAT TAT AAG TTA TG  
CGA TAT TGA AGC ATA TCG TAT GTA ATA TGC TTC AAT AC CTAG  
NcoI BamHI

B

MCS: CAT ATG CCC ATG GCT CGA GGA TCC GAA TTC  
NdeI NcoI BamHI XhoI EcoRI



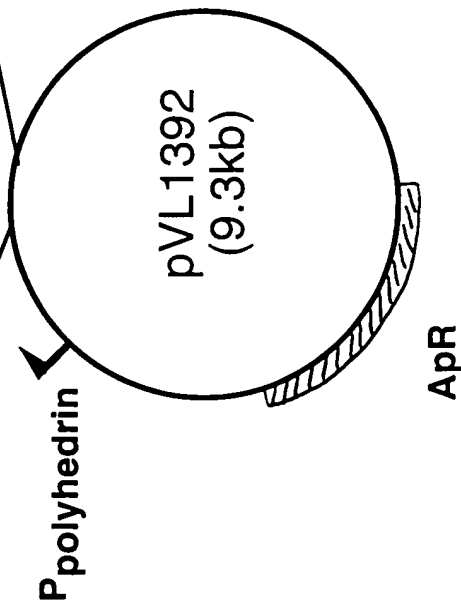
# Construction of pVL1392-lox:

A

Linker: GG CCG GAC GTC ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA TG  
 C CTG CAG TAT TGA AGC ATA TCG TAT GTA ATA TGC TTC AAT AC CTAG  
 NotI BamHI

B

MCS: BglII/PstI/NotI/XmaI/EcoRI/XbaI/SmaI/BamHI



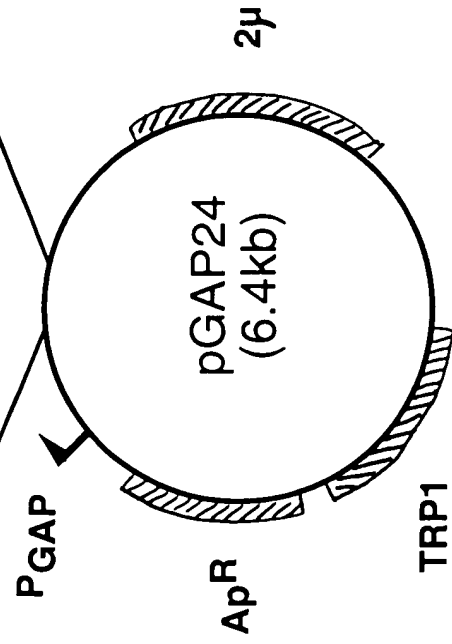
# Construction of pGAP24-lox:

**A**

Linker: T . CGA GAC GTC ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA TGC  
 CTG CAG TAT TGA AGC ATA TCG TAT GTA ATA TGC TTC AAT ACG CCGG  
 XhoI NotI

**B**

MCS: XhoI/BclI/NotI/EagI/StyI/AflII



# Construction of pGAL14-lox:

A

Linker: T CGA GAC GTC ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA TGC  
 CTG CAG TAT TGA AGC ATA TCG TAT CAT GTA ATA TGC TTC AAT ACG CCGG  
 XhoI NotI

B

MCS: SalI/ClaI/PstI/SmaI/XmaI/SpeI/NotI/EagI/SacII/SacI

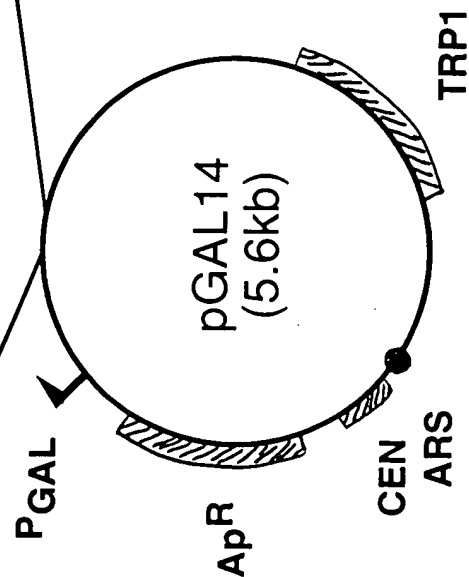
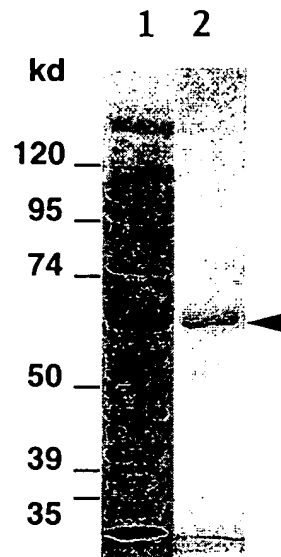


FIGURE 7



864240-4822160

FIGURE 8

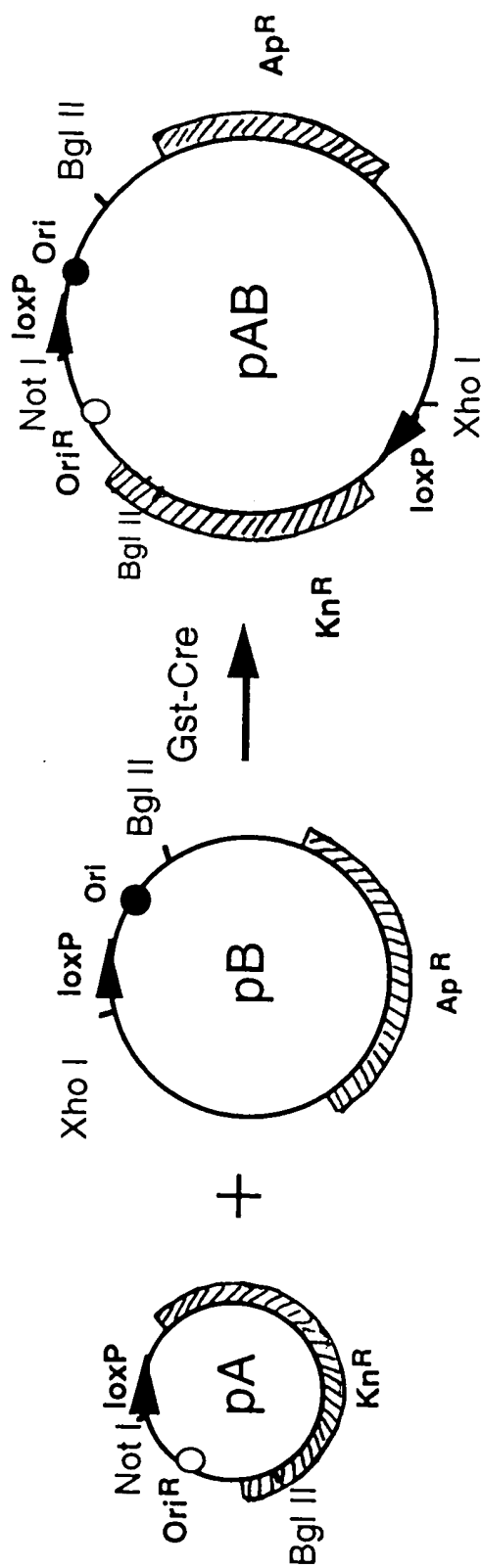
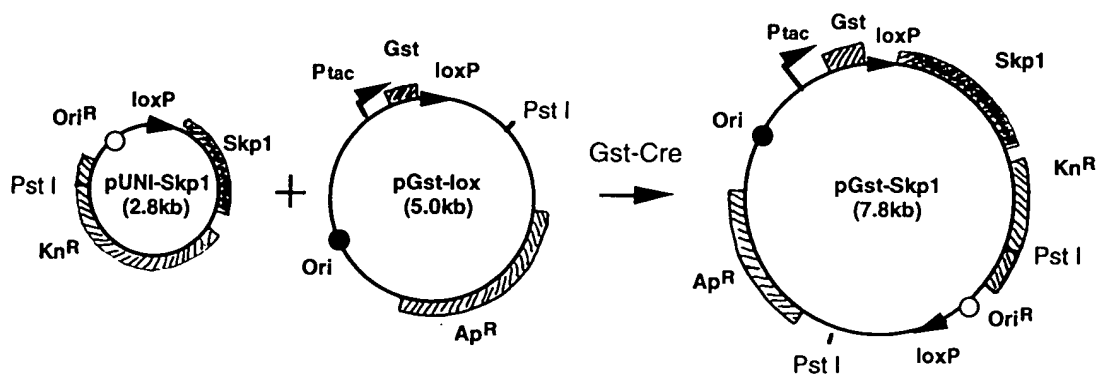




FIGURE 9

A



B

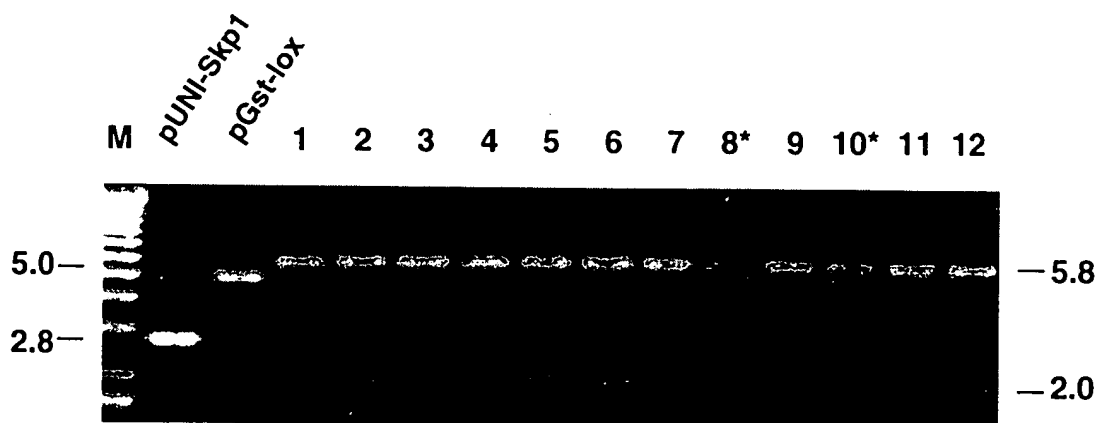
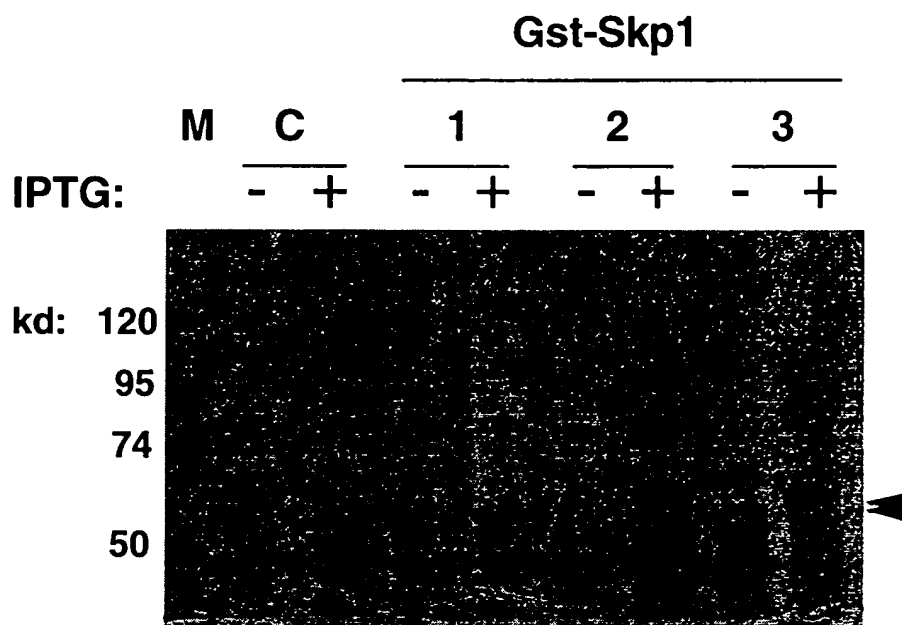


FIGURE 10

A



B

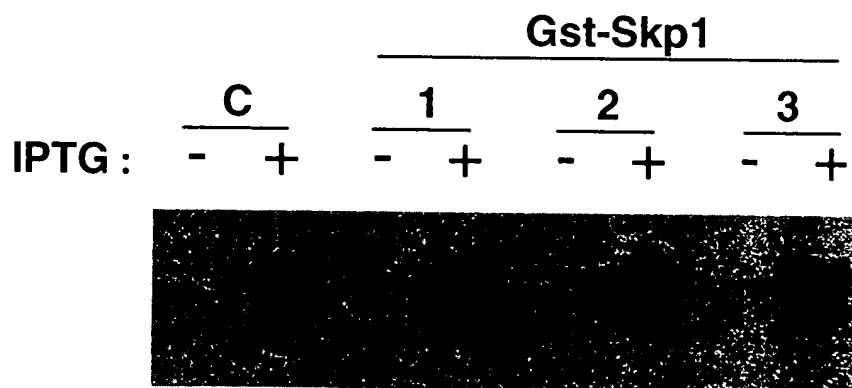
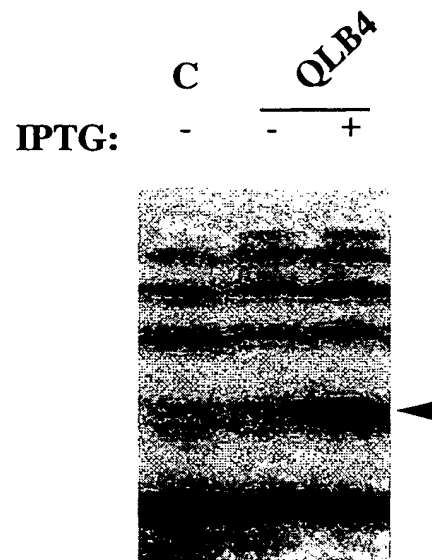
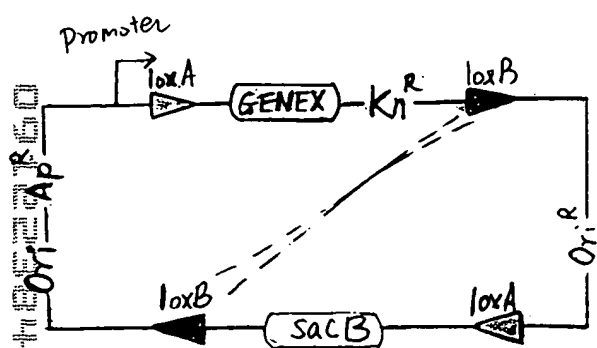
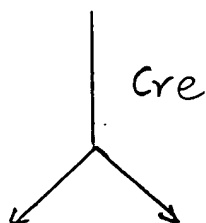
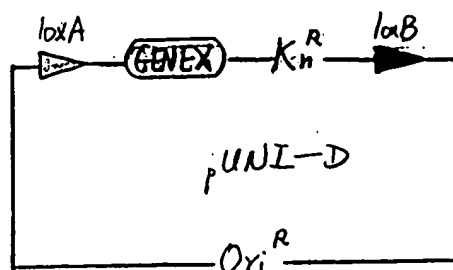
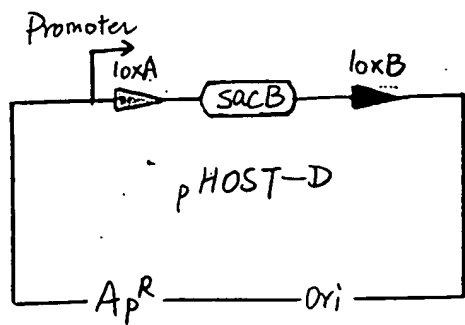


FIGURE 11

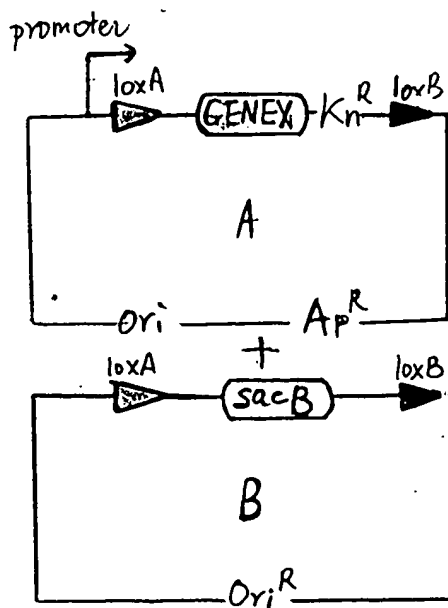
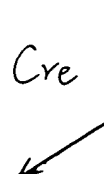
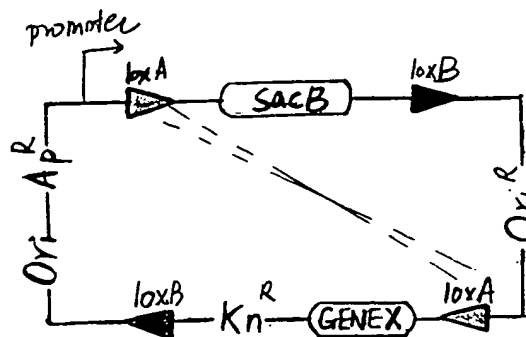


09122384-072498

FIGURE 12



OR



# FIGURE 13

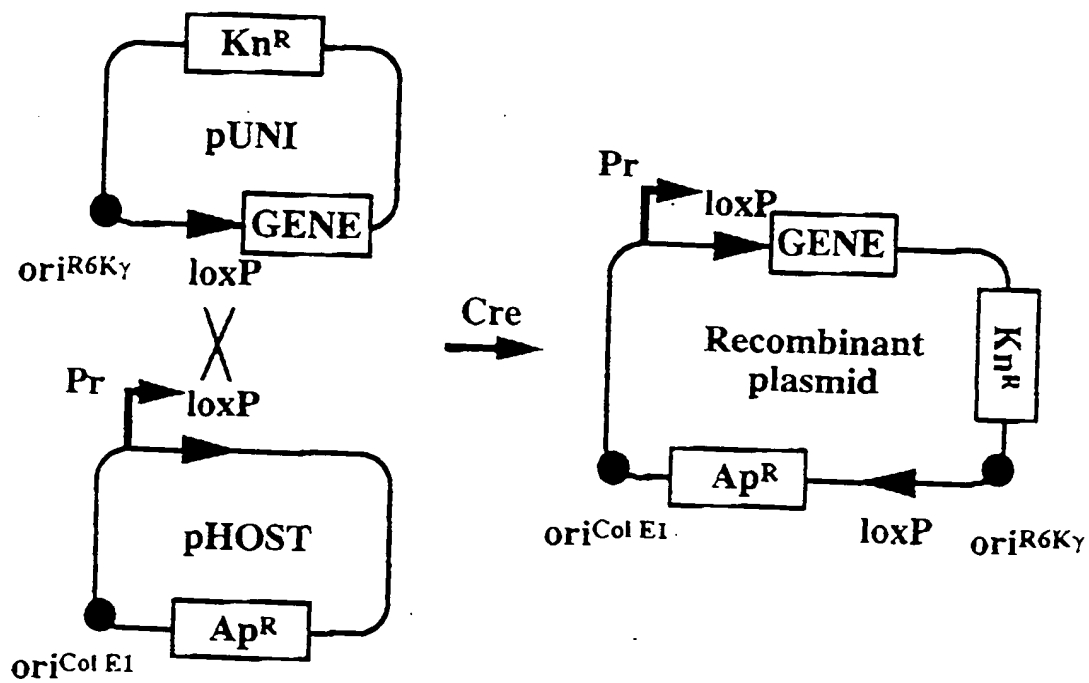
loxP:           ATAACTTCGTATA GCATACAT TATACGAAGTTAT  
                  1 2 3 4 5 6 7 8 9 10 11 12 13                   13 12 11 10 9 8 7 6 5 4 3 2 1

loxP2:           ATA**A**ACT**T**TCGTATA GCATACAT TATACGAAGTTAT  
                  1 2 3 4 5 6 7 8 9 10 11 12 13                   13 12 11 10 9 8 7 6 5 4 3 2 1

loxP3:           ATAACTTCGTATA GCATACAT TATA**C**GAAGTTAT  
                  1 2 3 4 5 6 7 8 9 10 11 12 13                   13 12 11 10 9 8 7 6 5 4 3 2 1

loxP23           ATA**A**ACT**T**TCGTATA GCATACAT TATA**C**GAAGTTAT  
                  1 2 3 4 5 6 7 8 9 10 11 12 13                   13 12 11 10 9 8 7 6 5 4 3 2 1

FIGURE 14



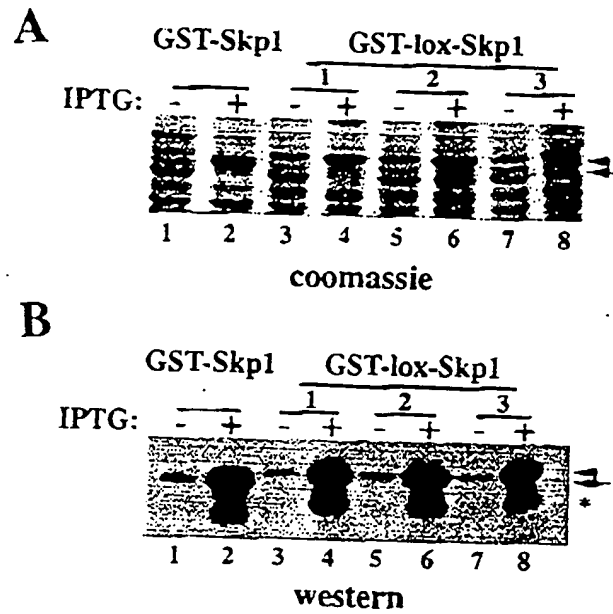
012334-07493  
054320-4882760

FIGURE 15

GST-Cre ( $\mu$ g)	number of Ap <sup>R</sup> transformants	number of Kn <sup>R</sup> transformants	Kn <sup>R</sup> /Ap <sup>R</sup> (%)
0	$4.0 \times 10^5$	0	0
0.02	$3.0 \times 10^5$	231	0.1
0.04	$2.3 \times 10^5$	406	0.2
0.06	$2.4 \times 10^5$	868	0.4
0.08	$3.3 \times 10^5$	1,336	0.4
0.10	$6.0 \times 10^4$	594	1.0
0.20	$7.8 \times 10^4$	580	0.7
0.40	$5.8 \times 10^4$	1,910	3.3
0.60	$9.2 \times 10^4$	10,750	11.7
0.80	$3.1 \times 10^5$	28,660	9.2
1.00	$1.0 \times 10^5$	16,840	16.8

964240-1822760

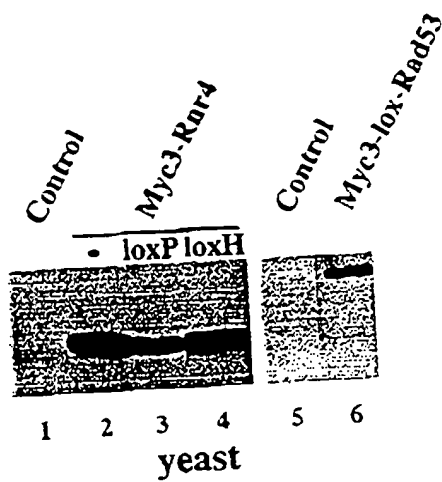
FIGURE 16



864240-48E22760



FIGURE 17



064240-48E22750

FIGURE 18

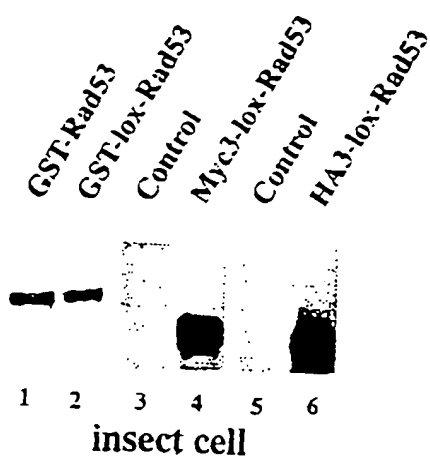
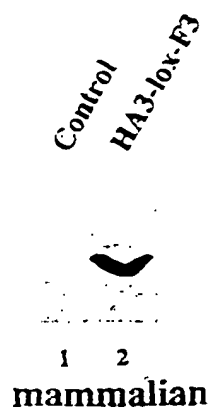
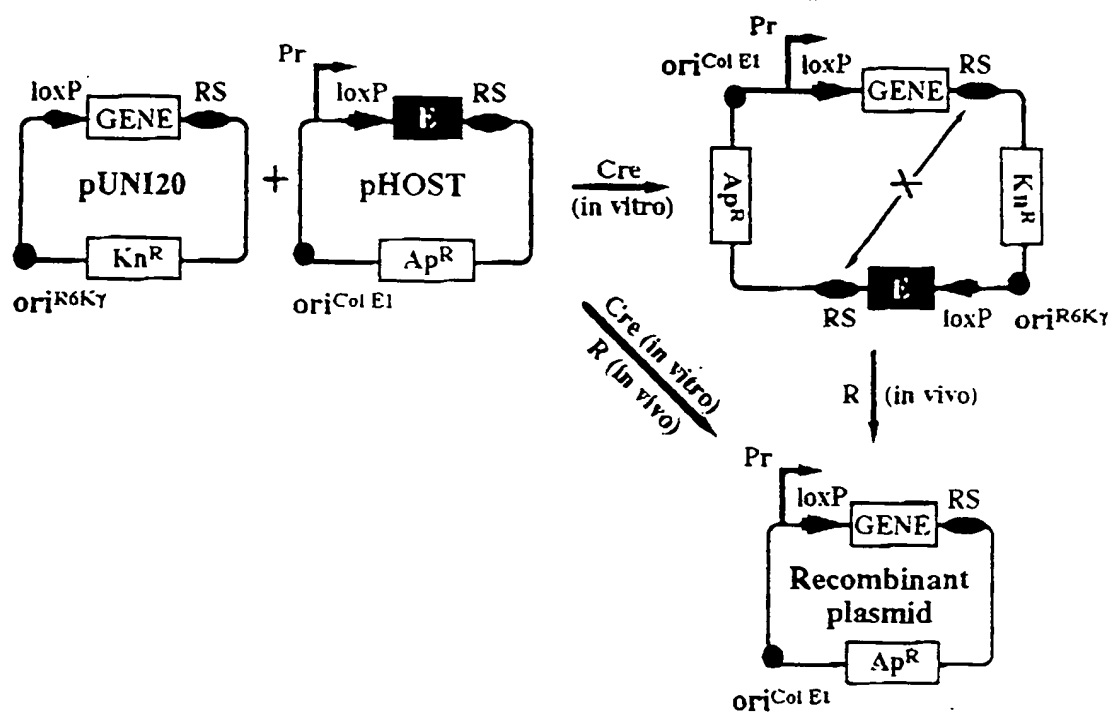


FIGURE 19



091227-04482260

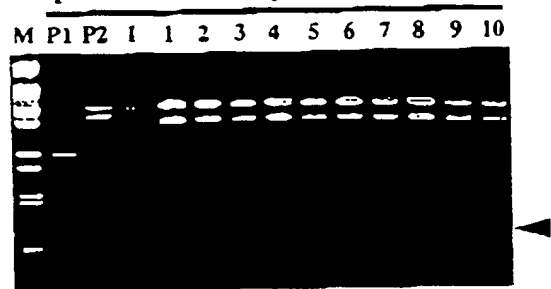
FIGURE 20



864240-48E22T60

FIGURE 21

Pvu II restriction analysis of recombinant  
plasmids made by one-step POT



091234-072498

FIGURE 22

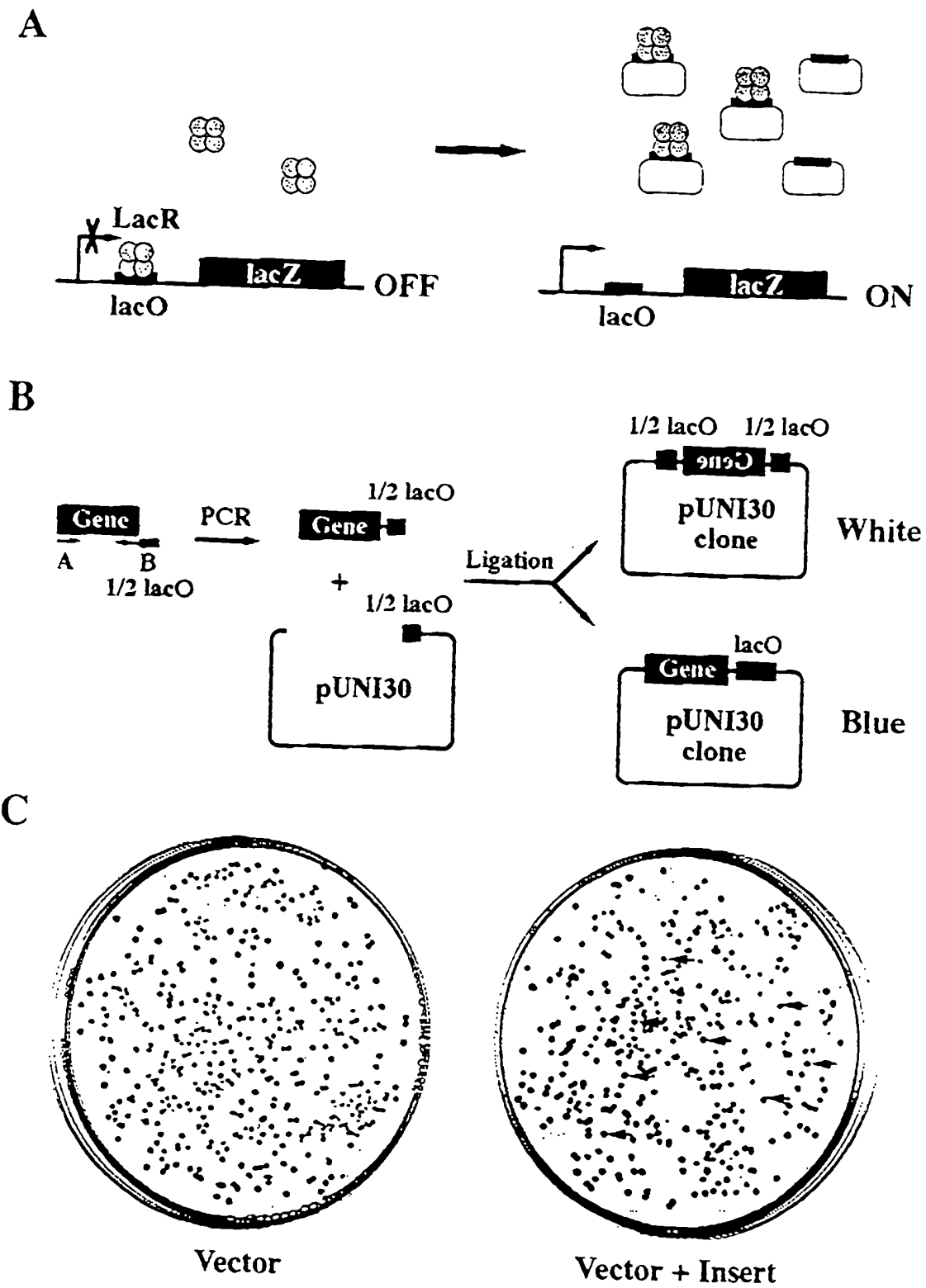
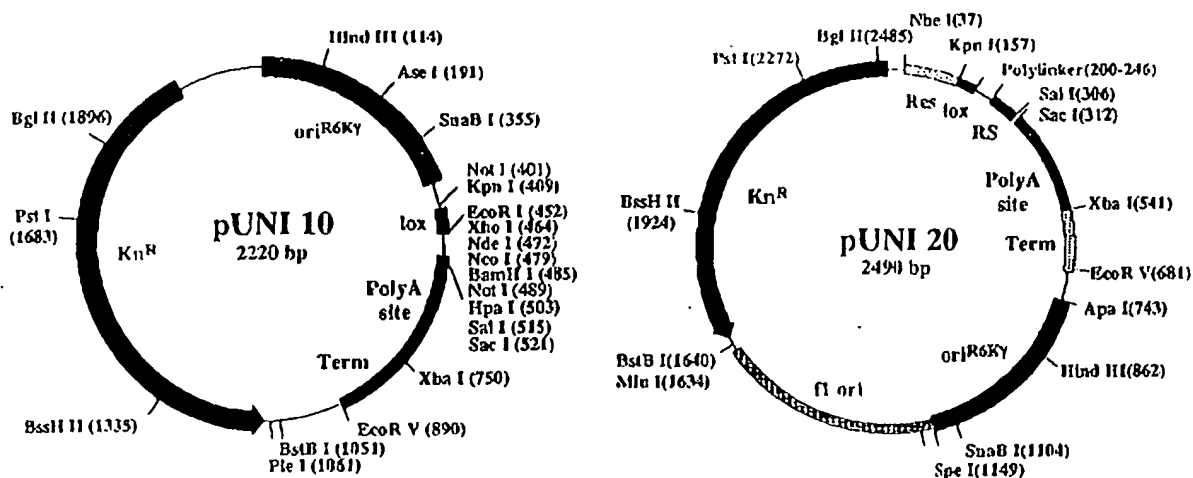


FIGURE 23



pUNI 10 Polylinker Sequence

(401) Not I      Kpn I      LOX  
GC GGC CGC GGT ACC ATA ACT TCG TAT AGC ATA CAT TAT ACG A

EcoR I      Sma I      Xho I      Nde I      Nco I  
AG TTA TCT GGA ATT CCC CGG GCT CGA GAA CAT ATG GCC ATG G

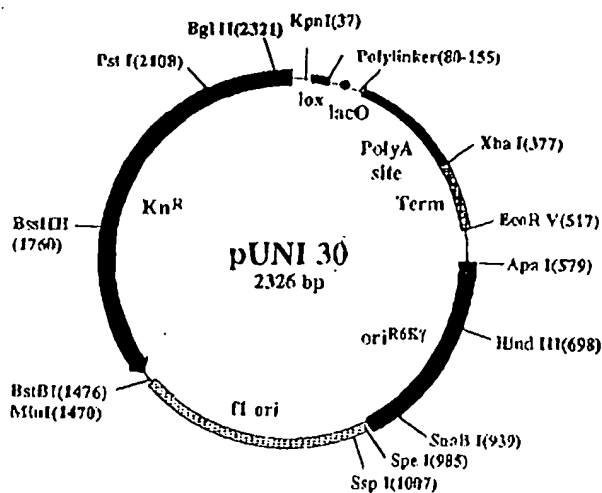
BamHI      Not I      Hpa I      Sal I      Sac I (530)  
GG ATC CGC GGC CGC AAT TGT TAA CAG ATC CGT CGA CGA GCT

pUNI 20 Polylinker Sequence

(157) Kpn I      LOX  
GGT ACC ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA T

EcoR I      Sma I      Xho I      Nde I      Nco I      BamHI  
CT GGA ATT CCC CGG GCT CGA GAACAT ATG GCC ATG GGG ATC

Not I (246)  
CGC GGC CGC



pUNI 30 Polylinker Sequence

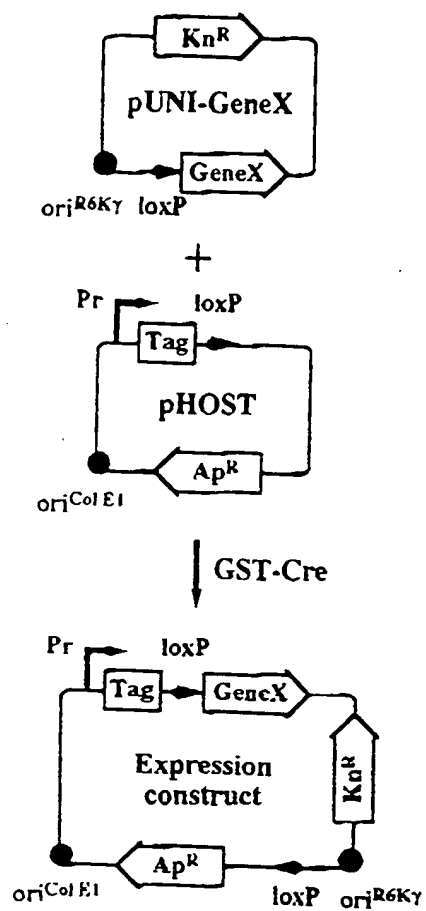
(37) Kpn I      LOX  
GGT ACC ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA TC

EcoR I      Sma I      Xho I      EcoRII  
T GGA ATT CCC CGG GCT CGA GCC AGT CCA CGC CTC ACA ATT  
half lacO

Not I      Hpa I      Sal I      Sac I (155)  
CGC GGC GCA ATT GTT AAC ACA TCC GTC GAC GAG CTC GC  
MunI

354220-422260

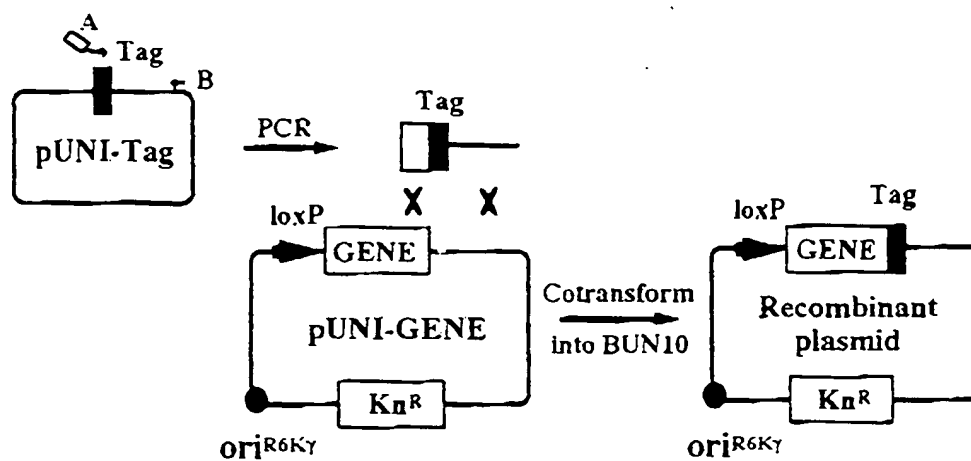
FIGURE 24



2022-04-22 10:22:22



FIGURE 25



0364240-48822760

## FIGURE 26A

SEQUENCE DESCRIPTION: SEQ ID NO:1:

AATTCTGTCA GCCGTTAAGT GTTCCTGTGT CACTGAAAAT TGCTTTGAGA GGCTCTAAGG  
60

GCTTCTCAGT GCGTTACATC CCTGGCTTGT TGTCCACAAC CGTTAAACCT TAAAAGCTTT  
120

AAAAGCCTTA TATATTCTTT TTTTCTTAT AAAACTTAAA ACCTTAGAGG CTATTTAAGT  
180

TGCTGATTTA TATTAATTTT ATTGTTCAAA CATGAGAGCT TAGTACGTGA AACATGAGAG  
240

CTTAGTACGT TAGCCATGAG AGCTTAGTAC GTTAGCCATG AGGGTTTAGT TCGTTAAACA  
300

TGAGAGCTTA GTACGTTAAA CATGAGAGCT TAGTACGTGA AACATGAGAG CTTAGTACGT  
360

ACTATCAACA GGTGAACTG CTGATCAACA GATCCTCTAC GCGGCCGCGG TACCATAACT  
420

TCGTATAGCA TACATTATAC GAAGTTATCT GGAATTCCCC GGGCTCGAGA ACATATGGCC  
480

ATGGGGATCC GCGGCCGCAA TTGTTAACAG ATCCGTCGAC GAGCTCGCTA TCAGCCTCGA  
540

CTGTGCCTTC TAGTTGCCAG CCATCTGTTG TTTGCCCCCTC CCCCCTGCCT TCCTTGACCC  
600

TGGAAGGTGC CACTCCCCT GTCTTTTCTT AATAAAATGA GGAAATTGCA TCGCATTGTC  
660

TGAGTAGGTG TCATTCTATT CTGGGGGGTG GGGTGGGGCA GGACAGCAAG GGGGAGGATT  
720

GGGAAGACAA TAGCAGGCAT GCTGGGGATT CTAGAAGATC CGGCTGCTAA CAAAGCCCGA  
780

AAGGAAGCTG AGTTGGCTGC TGCCACCGCT GAGCAATAAC TAGCATAACC CTTGGGGCC  
840

TCTAAACGGG TCTTGAGGGG TTTTTTGCTG AAAGGAGGAA CTATATCCGG ATATCCCGGG  
900

GTGGGCGAAG AACTCCAGCA TGAGATCCCC GCGCTGGAGG ATCATCCAGC CGGCGTCCCCG  
960

GAAAACGATT CCGAAGCCCA ACCTTTCATA GAAGGCGGCG GTGGAATCGA AATCTCGTGA  
1020

TGGCAGGTTG GCGGTCGCTT GGTCGGTCAT TTCGAACCCC AGAGTCCCGC TCAGAAGAAC  
1080

3642204322160

TCGTCAAGAA GGCGATAGAA GGCGATGCGC TGCGAATCGG GAGCGGCGAT ACCGTAAAGC  
1140

ACGAGGAAGC GGTCAGCCCA TTCGCCGCCA AGCTCTTCAG CAATATCACG GGTAGCCAAC  
1200

GCTATGTCCT GATAGCGGTC CGCCACACCC AGCCGGCCAC AGTCGATGAA TCCAGAAAAG  
1260

CGGCCATTTT CCACCATGAT ATTCGGCAAG CAGGCATCGC CATGGGTCAC GACGAGATCC  
1320

TCGCCGTCGG GCATGCGCGC CTTGAGCCTG GCGAACAGTT CGGCTGGCGC GAGCCCCTGA  
1380

TGCTCTTCGT CCAGATCATC CTGATCGACA AGACCGGCTT CCATCCGAGT ACGTGCTCGC  
1440

TCGATGCGAT GTTTCGCTTG GTGGTCGAAT GGGCAGGTAG CCGGATCAAG CGTATGCAGC  
1500

CGCCGCATTG CATCAGCCAT GATGGATACT TTCTCGGCAG GAGCAAGGTG AGATGACAGG  
1560

AGATCCTGCC CCGGCACTTC GCCCAATAGC AGCCAGTCCC TTCCCGCTTC AGTGACAACG  
1620

TCGAGCACAG CTGCGCAAGG AACGCCCCGTC GTGGCCAGCC ACGATAGCCG CGCTGCCTCG  
1680

TCCTGCAGTT CATTCAAGGC ACCGGACAGG TCGGTCTTGA CAAAAGAAGC CGGGCGCCCC  
1740

TGCGCTGACA GCCGGAACAC GGCGGCATCA GAGCAGCCGA TTGTCTGTTG TGCCCAAGTCA  
1800

TAGCCGAATA GCCTCTCCAC CCAAGCGGCC GGAGAACCTG CGTGCAATCC ATCTTGTTCA  
1860

ATCATGCGAA ACGATCCTCA TCCTGTCTCT TGATCAGATC TTGATCCCCT GCGCCATCAG  
1920

ATCCTTGGCG GCAAGAAAGC CATCCAGTTT ACTTTGCAGG GCTTCCCAAC CTTACCAGAG  
1980

GGCGCCCCAG CTGGCAATTC CGGTTCGCTT GCTGTCCATA AAACCGCCCA GTCTAGCTAT  
2040

CGCCATGTAA GCCCACTGCA AGCTACCTGC TTTCTCTTTG CGCTTGCGTT TTCCCTTGTC  
2100

36420-482260

CAGATAGCCC AGTAGCTGAC ATTCATCCGG GGTCAGCACC GTTCTGCGG ACTGGCTTTC  
2160

TACGTGTTCC GCTTCCTTTA GCAGCCCTTG CGCCCTGAGT GCTTGCGGCA GCGTGAAGCT  
2220

364220-4362760

# FIGURE 26B

SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG	TCC	CCT	ATA	CTA	GGT	TAT	TGG	AAA	ATT	AAG	GGC	CTT	GTG	CAA	CCC	48
Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro	
1				5					10					15		
ACT	CGA	CTT	CTT	TTG	GAA	TAT	CTT	GAA	GAA	AAA	TAT	GAA	GAG	CAT	TTG	96
Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu	
			20					25					30			
TAT	GAG	CGC	GAT	GAA	GGT	GAT	AAA	TGG	CGA	AAC	AAA	AAG	TTT	GAA	TTG	144
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu	
		35					40					45				
GGT	TTG	GAG	TTT	CCC	AAT	CTT	CCT	TAT	TAT	ATT	GAT	GGT	GAT	GTT	AAA	192
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	
	50					55					60					
TTA	ACA	CAG	TCT	ATG	GCC	ATC	ATA	CGT	TAT	ATA	GCT	GAC	AAG	CAC	AAC	240
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	
65					70					75					80	
ATG	TTG	GGT	GGT	TGT	CCA	AAA	GAG	CGT	GCA	GAG	ATT	TCA	ATG	CTT	GAA	288
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	
				85					90					95		
GGA	GCG	GTT	TTG	GAT	ATT	AGA	TAC	GGT	GTT	TCG	AGA	ATT	GCA	TAT	AGT	336
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	
			100					105					110			
AAA	GAC	TTT	GAA	ACT	CTC	AAA	GTT	GAT	TTT	CTT	AGC	AAG	CTA	CCT	GAA	384
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
		115					120					125				
ATG	CTG	AAA	ATG	TTC	GAA	GAT	CGT	TTA	TGT	CAT	AAA	ACA	TAT	TTA	AAT	432
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
	130					135					140					
GGT	GAT	CAT	GTA	ACC	CAT	CCT	GAC	TTC	ATG	TTG	TAT	GAC	GCT	CTT	GAT	480
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
145					150					155					160	

964340-4322150

GTT 528	GTT	TTA	TAC	ATG	GAC	CCA	ATG	TGC	CTG	GAT	GCG	TTC	CCA	AAA	TTA
Val	Val	Leu	Tyr	Met 165	Asp	Pro	Met	Cys	Leu 170	Asp	Ala	Phe	Pro	Lys 175	Leu
GTT 576	TGT	TTT	AAA	AAA	CGT	ATT	GAA	GCT	ATC	CCA	CAA	ATT	GAT	AAG	TAC
Val	Cys	Phe	Lys 180	Lys	Arg	Ile	Glu	Ala 185	Ile	Pro	Gln	Ile	Asp 190	Lys	Tyr
TTG 624	AAA	TCC	AGC	AAG	TAT	ATA	GCA	TGG	CCT	TTG	CAG	GGC	TGG	CAA	GCC
Leu	Lys	Ser 195	Ser	Lys	Tyr	Ile	Ala 200	Trp	Pro	Leu	Gln	Gly 205	Trp	Gln	Ala
ACG 672	TTT	GGT	GGT	GGC	GAC	CAT	CCT	CCA	AAA	TCG	GAT	CTG	GTT	CCG	CGT
Thr	Phe 210	Gly	Gly	Gly	Asp	His 215	Pro	Pro	Lys	Ser	Asp 220	Leu	Val	Pro	Arg
GGA 720	TCT	CGT	CGT	GCA	TCT	GTT	GGA	TCG	CAT	ATG	CCC	ATG	GCC	AAT	TTA
Gly 225	Ser	Arg	Arg	Ala	Ser 230	Val	Gly	Ser	His	Met 235	Pro	Met	Ala	Asn	Leu 240
CTG 768	ACC	GTA	CAC	CAA	AAT	TTG	CCT	GCA	TTA	CCG	GTC	GAT	GCA	ACG	AGT
Leu	Thr	Val	His	Gln 245	Asn	Leu	Pro	Ala	Leu 250	Pro	Val	Asp	Ala	Thr 255	Ser
GAT 816	GAG	GTT	CGC	AAG	AAC	CTG	ATG	GAC	ATG	TTC	AGG	GAT	CGC	CAG	GCG
Asp	Glu	Val	Arg 260	Lys	Asn	Leu	Met	Asp 265	Met	Phe	Arg	Asp	Arg 270	Gln	Ala
TTT 864	TCT	GAG	CAT	ACC	TGG	AAA	ATG	CTT	CTG	TCC	GTT	TGC	CGG	TCG	TGG
Phe	Ser	Glu 275	His	Thr	Trp	Lys	Met 280	Leu	Leu	Ser	Val	Cys 285	Arg	Ser	Trp
GCG 912	GCA	TGG	TGC	AAG	TTG	AAT	AAC	CGG	AAA	TGG	TTT	CCC	GCA	GAA	CCT
Ala	Ala 290	Trp	Cys	Lys	Leu	Asn 295	Asn	Arg	Lys	Trp	Phe 300	Pro	Ala	Glu	Pro
GAA 960	GAT	GTT	CGC	GAT	TAT	CTT	CTA	TAT	CTT	CAG	GCG	CGC	GGT	CTG	GCA
Glu 305	Asp	Val	Arg	Asp	Tyr 310	Leu	Leu	Tyr	Leu	Gln 315	Ala	Arg	Gly	Leu	Ala 320
GTA 1008	AAA	ACT	ATC	CAG	CAA	CAT	TTG	GGC	CAG	CTA	AAC	ATG	CTT	CAT	CGT
Val	Lys	Thr	Ile	Gln 325	Gln	His	Leu	Gly	Gln 330	Leu	Asn	Met	Leu	His 335	Arg
CGG 1056	TCC	GGG	CTG	CCA	CGA	CCA	AGT	GAC	AGC	AAT	GCT	GTT	TCA	CTG	GTT
Arg	Ser	Gly	Leu 340	Pro	Arg	Pro	Ser	Asp 345	Ser	Asn	Ala	Val	Ser 350	Leu	Val

ATG	CGG	CGG	ATC	CGA	AAA	GAA	AAC	GTT	GAT	GCC	GGT	GAA	CGT	GCA	AAA
1104															
Met	Arg	Arg	Ile	Arg	Lys	Glu	Asn	Val	Asp	Ala	Gly	Glu	Arg	Ala	Lys
		355					360					365			
CAG	GCT	CTA	GCG	TTC	GAA	CGC	ACT	GAT	TTC	GAC	CAG	GTT	CGT	TCA	CTC
1152															
Gln	Ala	Leu	Ala	Phe	Glu	Arg	Thr	Asp	Phe	Asp	Gln	Val	Arg	Ser	Leu
	370					375					380				
ATG	GAA	AAT	AGC	GAT	CGC	TGC	CAG	GAT	ATA	CGT	AAT	CTG	GCA	TTT	CTG
1200															
Met	Glu	Asn	Ser	Asp	Arg	Cys	Gln	Asp	Ile	Arg	Asn	Leu	Ala	Phe	Leu
385					390					395					400
GGG	ATT	GCT	TAT	AAC	ACC	CTG	TTA	CGT	ATA	GCC	GAA	ATT	GCC	AGG	ATC
1248															
Gly	Ile	Ala	Tyr	Asn	Thr	Leu	Leu	Arg	Ile	Ala	Glu	Ile	Ala	Arg	Ile
				405					410					415	
AGG	GTT	AAA	GAT	ATC	TCA	CGT	ACT	GAC	GGT	GGG	AGA	ATG	TTA	ATC	CAT
1296															
Arg	Val	Lys	Asp	Ile	Ser	Arg	Thr	Asp	Gly	Gly	Arg	Met	Leu	Ile	His
			420					425					430		
ATT	GGC	AGA	ACG	AAA	ACG	CTG	GTT	AGC	ACC	GCA	GGT	GTA	GAG	AAG	GCA
1344															
Ile	Gly	Arg	Thr	Lys	Thr	Leu	Val	Ser	Thr	Ala	Gly	Val	Glu	Lys	Ala
		435					440					445			
CTT	AGC	CTG	GGG	GTA	ACT	AAA	CTG	GTC	GAG	CGA	TGG	ATT	TCC	GTC	TCT
1392															
Leu	Ser	Leu	Gly	Val	Thr	Lys	Leu	Val	Glu	Arg	Trp	Ile	Ser	Val	Ser
	450					455					460				
GGT	GTA	GCT	GAT	GAT	CCG	AAT	AAC	TAC	CTG	TTT	TGC	CGG	GTC	AGA	AAA
1440															
Gly	Val	Ala	Asp	Asp	Pro	Asn	Asn	Tyr	Leu	Phe	Cys	Arg	Val	Arg	Lys
465					470					475					480
AAT	GGT	GTT	GCC	GCG	CCA	TCT	GCC	ACC	AGC	CAG	CTA	TCA	ACT	CGC	GCC
1488															
Asn	Gly	Val	Ala	Ala	Pro	Ser	Ala	Thr	Ser	Gln	Leu	Ser	Thr	Arg	Ala
				485					490					495	
CTG	GAA	GGG	ATT	TTT	GAA	GCA	ACT	CAT	CGA	TTG	ATT	TAC	GGC	GCT	AAG
1536															
Leu	Glu	Gly	Ile	Phe	Glu	Ala	Thr	His	Arg	Leu	Ile	Tyr	Gly	Ala	Lys
			500					505					510		
GAT	GAC	TCT	GGT	CAG	AGA	TAC	CTG	GCC	TGG	TCT	GGA	CAC	AGT	GCC	CGT
1584															
Asp	Asp	Ser	Gly	Gln	Arg	Tyr	Leu	Ala	Trp	Ser	Gly	His	Ser	Ala	Arg
		515					520					525			
GTC	GGA	GCC	GCG	CGA	GAT	ATG	GCC	CGC	GCT	GGA	GTT	TCA	ATA	CCG	GAG
1632															
Val	Gly	Ala	Ala	Arg	Asp	Met	Ala	Arg	Ala	Gly	Val	Ser	Ile	Pro	Glu
	530					535					540				

ATC ATG CAA GCT GGT GGC TGG ACC AAT GTA AAT ATT GTC ATG AAC TAT  
1680  
Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile Val Met Asn Tyr  
545 550 555 560

ATC CGT AAC CTG GAT AGT GAA ACA GGG GCA ATG GTG CGC CTG CTG GAA  
1728  
Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val Arg Leu Leu Glu  
565 570 575

GAT GGC GAT TAG  
1740  
Asp Gly Asp

364220-4862760



# FIGURE 26C

SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro			
1				5					10					15				
Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu			
			20					25					30					
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu			
		35					40					45						
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys			
	50					55					60							
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn			
65					70					75					80			
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu			
				85					90					95				
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser			
			100					105					110					
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu			
		115					120					125						
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn			
	130					135					140							
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp			
145					150					155					160			
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu			
				165					170					175				
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr			
			180					185					190					
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala			
		195					200					205						
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg			
	210					215					220							
Gly	Ser	Arg	Arg	Ala	Ser	Val	Gly	Ser	His	Met	Pro	Met	Ala	Asn	Leu			
225					230					235					240			
Leu	Thr	Val	His	Gln	Asn	Leu	Pro	Ala	Leu	Pro	Val	Asp	Ala	Thr	Ser			
				245					250					255				
Asp	Glu	Val	Arg	Lys	Asn	Leu	Met	Asp	Met	Phe	Arg	Asp	Arg	Gln	Ala			
			260					265					270					
Phe	Ser	Glu	His	Thr	Trp	Lys	Met	Leu	Leu	Ser	Val	Cys	Arg	Ser	Trp			

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275					280					285					
Ala	Ala	Trp	Cys	Lys	Leu	Asn	Asn	Arg	Lys	Trp	Phe	Pro	Ala	Glu	Pro
	290					295					300				
Glu	Asp	Val	Arg	Asp	Tyr	Leu	Leu	Tyr	Leu	Gln	Ala	Arg	Gly	Leu	Ala
305					310					315					320
Val	Lys	Thr	Ile	Gln	Gln	His	Leu	Gly	Gln	Leu	Asn	Met	Leu	His	Arg
				325					330					335	
Arg	Ser	Gly	Leu	Pro	Arg	Pro	Ser	Asp	Ser	Asn	Ala	Val	Ser	Leu	Val
			340					345					350		
Met	Arg	Arg	Ile	Arg	Lys	Glu	Asn	Val	Asp	Ala	Gly	Glu	Arg	Ala	Lys
		355					360					365			
Gln	Ala	Leu	Ala	Phe	Glu	Arg	Thr	Asp	Phe	Asp	Gln	Val	Arg	Ser	Leu
	370					375					380				
Met	Glu	Asn	Ser	Asp	Arg	Cys	Gln	Asp	Ile	Arg	Asn	Leu	Ala	Phe	Leu
385					390					395					400
Gly	Ile	Ala	Tyr	Asn	Thr	Leu	Leu	Arg	Ile	Ala	Glu	Ile	Ala	Arg	Ile
				405					410					415	
Arg	Val	Lys	Asp	Ile	Ser	Arg	Thr	Asp	Gly	Gly	Arg	Met	Leu	Ile	His
			420					425					430		
Ile	Gly	Arg	Thr	Lys	Thr	Leu	Val	Ser	Thr	Ala	Gly	Val	Glu	Lys	Ala
		435					440					445			
Leu	Ser	Leu	Gly	Val	Thr	Lys	Leu	Val	Glu	Arg	Trp	Ile	Ser	Val	Ser
	450					455					460				
Gly	Val	Ala	Asp	Asp	Pro	Asn	Asn	Tyr	Leu	Phe	Cys	Arg	Val	Arg	Lys
465					470					475					480
Asn	Gly	Val	Ala	Ala	Pro	Ser	Ala	Thr	Ser	Gln	Leu	Ser	Thr	Arg	Ala
				485					490					495	
Leu	Glu	Gly	Ile	Phe	Glu	Ala	Thr	His	Arg	Leu	Ile	Tyr	Gly	Ala	Lys
			500					505					510		
Asp	Asp	Ser	Gly	Gln	Arg	Tyr	Leu	Ala	Trp	Ser	Gly	His	Ser	Ala	Arg
		515					520					525			
Val	Gly	Ala	Ala	Arg	Asp	Met	Ala	Arg	Ala	Gly	Val	Ser	Ile	Pro	Glu
	530					535					540				
Ile	Met	Gln	Ala	Gly	Gly	Trp	Thr	Asn	Val	Asn	Ile	Val	Met	Asn	Tyr
545					550					555					560
Ile	Arg	Asn	Leu	Asp	Ser	Glu	Thr	Gly	Ala	Met	Val	Arg	Leu	Leu	Glu
				565					570					575	
Asp	Gly	Asp													